IN THE CLAIMS:

Please amend Claims 2 to 5 and 10 as shown below.

1. (Cancelled)

2. (Currently Amended) A method for identifying a base sequence present in a target single-stranded nucleic acid comprising the steps of:

(a) preparing a probe array in which single-stranded nucleic acid probes of No. 1 to No. n ($n \geq 3$) are arranged as isolated spots on a substrate;

(b) reacting a single-stranded nucleic acid which has a base sequence fully complementary to a base sequence of one of the single-stranded nucleic acid probes and is fluorescence-labeled, with the probe array under such conditions that single-stranded nucleic acids complementary to each other form a double-stranded nucleic acid;

removing the unreacted labeled single-stranded nucleic acid; and

measuring fluorescence intensity of each spot of the probe array to obtain a first template pattern showing a relationship between location of the probes and fluorescent characteristics;

(c) analyzing the first template pattern to locate probes and to calculate a mean value of fluorescence intensities (Fi) of the double-stranded nucleic acids having i of mismatched base pairs, where i is an integer not less than 1;

(d) calculating a difference (F1, 0) between a mean value of ~~the~~ fluorescence ~~intensity~~ intensities of the fully complementary double-stranded nucleic ~~acid~~ acids without mismatch (F0) and ~~the~~ a mean value of ~~the~~ fluorescence intensities of ~~the~~

double-stranded nucleic acids having one-base mismatch (F1), further calculating a difference (Fi+1, i) between a mean value of fluorescence ~~intensity~~ intensities of a double-stranded nucleic acid having (i+1) base mismatches (Fi+1) and [[a]] the mean value of the fluorescence ~~intensity~~ intensities of [[a]] the double-stranded nucleic ~~acid~~ acids having i-base mismatches (Fi), and identifying i being Fi+1, i << Fi, i-1;

(e) preparing a second template pattern of positive probe spots of probes having base sequences differing from the base sequence of the second probe by i or less bases where i is determined in said step (d), wherein negative probe spots are probes having base sequences differing from the second probe by more than i bases;

(f) performing the same operation as the step (e) for each of remaining single-stranded nucleic acid probes and obtaining template patterns of No. 3 to No. n showing a relationship between location and fluorescent characteristics of the probes;

(g) performing the same operation as the step (b) using a sample containing the target single-stranded nucleic acid of the base sequence to obtain a sample pattern showing a relationship between a position and fluorescent characteristics;

(h) comparing the sample pattern obtained in the step (g) with a plurality of template patterns, the plurality of template patterns comprising the first and second template patterns and the template patterns of No. 3 to No. n, to find a template pattern substantially identical to the sample pattern; and

(i) determining the base sequence of the target single-stranded nucleic acid to be a base sequence complementary to the base sequence of the probe taken for the preparation of the template pattern found in the step (h).

3. (Currently Amended) The method according to claim 2, wherein the step (g) further comprises the substep of obtaining a two-valued pattern of ~~the~~ fluorescence intensity by using the mean value of fluorescence ~~intensity~~ intensities (Fi) as a threshold intensity.

4. (Currently Amended) The method according to claim 2, wherein the length of each of the ~~probe~~ single-stranded nucleic acid probes is 8 mer to 30 mer.

5. (Currently Amended) The method according to claim 4, wherein the length of each of the ~~probe~~ single-stranded nucleic acid probes is 12 mer to 25 mer.

6. (Original) The method according to claim 2, wherein the number of the mismatched base pairs (i) is 1.

7 to 9. (Cancelled)

10. (Currently Amended) A method for identifying a base sequence present in a target nucleic acid by using a DNA chip in which a plurality of probes are arranged, comprising the steps of:

reacting a target nucleic acid which has a known base sequence and is fluorescence-labeled, with the DNA chip and then observing the DNA chip after the reaction to obtain a template pattern showing a relationship between the probe location and the fluorescence intensity;

reacting a target nucleic acid which has an unknown base sequence and is fluorescence-labeled, with the DNA chip and then observing the DNA chip after the reaction to obtain a sample pattern showing a relationship between the probe location and the fluorescence intensity; and

comparing the sample pattern with the template pattern to thereby determine whether the unknown base sequence agrees with the known base sequence,

wherein a threshold value is set up between a fluorescence intensity corresponding to i base mismatch(es) and a fluorescence intensity corresponding to i+1 base mismatches based on a difference between a mean value of fluorescence intensities of i-base mismatches and a mean value of fluorescence intensities of i+1 mismatches, where i is an integer not less than 1, such that a probe location showing a fluorescence intensity above the threshold value is defined to be positive while a probe location otherwise is defined to be negative, and the template pattern and the sample pattern are prepared by adopting only positive probe locations.

11. (Previously Presented) The method according to claim 10, wherein i is 1.